

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2001, 16:50:10 ; Search time 28.15 Seconds
(without alignments)
1823.860 Million cell updates/sec

Title: US-09-830-647-1

Perfect score: 3510
Sequence: 1 MNSGAMRHSHKGFHGGSIQV.....SDNLTAFSSPSSTFTGF 674

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3124	89.0	601	2 T02633	hypothetical prote
2	187	5.3	1790	2 S67583	transport protein
3	178	5.1	1642	2 T08880	NMDA receptor-blind
4	173	4.9	1365	2 T30822	Imp1 protein - Myc
5	170.5	4.9	911	2 S51441	hypothetical prote
6	170	4.8	1516	2 E71619	RAD2 endonuclease
7	166.5	4.7	1871	2 D96796	probable heat shock
8	165	4.7	1119	2 B70126	surface-located me
9	164.5	4.7	2401	2 T28676	rhoptery protein -
10	164	4.7	646	2 E71620	hypothetical prote
11	162	4.6	2269	2 T28677	rhoptery protein -
12	161	4.6	1300	2 T53799	CGI protein - huma
13	161	4.6	1356	2 S32763	kinectin 1 - human
14	159.5	4.5	1392	2 A43336	microtubule-vesicl
15	159.5	4.5	1427	2 S22685	reslin - human
16	158	4.5	980	2 E71606	hypothetical prote
17	158	4.5	1271	2 A45555	glutamate rich pro
18	157.5	4.5	1979	2 C71622	hypothetical prote
19	157.5	4.5	3488	2 T34418	hypothetical prote
20	156.5	4.5	1690	2 T13030	microtubule bindin
21	155.5	4.4	1056	2 S55151	probable membrane
22	155.5	4.4	1577	2 T19722	hypothetical prote
23	154.5	4.4	1211	2 T27522	hypothetical prote
24	154	4.4	2663	1 T24806	centromere protein
25	153.5	4.4	1164	2 T24806	hypothetical prote
26	152.5	4.3	1017	2 PC4035	cell-cycle-depende
27	152.5	4.3	1115	2 T41342	probable coiled-co
28	152.5	4.3	1738	2 T14867	interleptin - slime
29	152.5	4.3	3259	1 A56539	glantin - human

30	152	4.3	1312	1 BMBYDL	RAD50 protein - ye
31	152	4.3	1960	2 S34307	myosin heavy chain
32	151.5	4.3	1005	2 A64465	hypothetical prote
33	151.5	4.3	1039	2 S62509	probable vesicular
34	151.5	4.3	1044	2 T50213	probable vesicular
35	151.5	4.3	2104	2 T38774	myosin-3 heavy cha
36	151.5	4.3	3147	2 T18674	hypothetical prote
37	150.5	4.3	1127	2 T28317	ORF MSY156 hypothe
38	150.5	4.3	1313	2 F96673	hypothetical prote
39	150.5	4.3	1726	2 A45948	major mezoote su
40	150.5	4.3	1837	2 T41023	probable nuclear p
41	149.5	4.3	1088	2 T18559	hypothetical prote
42	149.5	4.3	1231	2 S70553	chromosome-associa
43	149.5	4.3	1726	1 SA2OGM	major mezoote su
44	149	4.2	1650	2 T18444	hypothetical prote
45	149	4.2	2245	2 T18278	myosin heavy chain

ALIGNMENTS

Query Match	Score	DB 2	Length	601
Best Local Similarity	100.0%	Pred. No. 1.8e-166		
Matches 601	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	74	RVEEFLSKDISYLSNKKKFAKFAOTLGRISPPSPESAVTAETSPHSHDGSFSPPT	133	
DB	1	RVEEFLSKDISYLSNKKKFAKFAOTLGRISPPSPESAVTAETSPHSHDGSFSPPT	60	
QY	134	VCLSRKLLVERKAIDHDFIPSNLSISNALSWGKILHIDIRYIEQKKELYLKSS	193	
DB	61	VCLSRKLLVERKAIDHDFIPSNLSISNALSWGKILHIDIRYIEQKKELYLKSS	120	
QY	194	TSVRGGKRVGSGAKTRGRKPKPVKVEDMSOLYRPYLOLTNNPFTNYSIQKCSFP	253	
DB	121	TSVRGGKRVGSGAKTRGRKPKPVKVEDMSOLYRPYLOLTNNPFTNYSIQKCSFP	180	
QY	254	DVDKPSMQQYQVVKLIOTPDGDKYGTSTIOLLEKKKKGGCECLOKYEDELTHLSE	313	
DB	181	DVDKPSMQQYQVVKLIOTPDGDKYGTSTIOLLEKKKKGGCECLOKYEDELTHLSE	240	
QY	314	QHRNFAOSNQYVDDIVSKLVDFEVEYEKDPKKRRIRYSGSLSPVASYLKTEQKE	373	
DB	241	QHRNFAOSNQYVDDIVSKLVDFEVEYEKDPKKRRIRYSGSLSPVASYLKTEQKE	300	
QY	374	KVELHISQKQDQEDTYKQNFILYKEQTEKKILFTISEIPRPSNLRGLNKKMSK	433	
DB	301	KVELHISQKQDQEDTYKQNFILYKEQTEKKILFTISEIPRPSNLRGLNKKMSK	360	
QY	434	CSMLSTAEDDIRQNTPLPHKKNQECILDISHTLSENDELRLVDHVKCNQASVHS	493	
DB	361	CSMLSTAEDDIRQNTPLPHKKNQECILDISHTLSENDELRLVDHVKCNQASVHS	420	


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      :      :      :      :      :      :      :      :      :      :
Db 409 LMGVLELQKRNHDSOFEPDIYORMEOETQKLEQLRAELD-EMYGQOYQAKMQLIRQ 467
      :      :      :      :      :      :      :      :      :      :
QY 286 ---QJKEKK---KKGYCECCLOKYEDELTH-----LSEOHNRNPAOSNQ----- 323
      :      :      :      :      :      :      :      :      :      :
Db 468 HMAQMEBKTRHKGEMENALRSYNTIVNEQDKLMVVAIINELNIKLQDTNSQKELKEE 527
      :      :      :      :      :      :      :      :      :      :
QY 324 -----YQVVDIVSKIVF--DPEVEKDTPKKKRKRY-----SVGSLSPVASV 365
      :      :      :      :      :      :      :      :      :      :
Db 528 LGLILEKCALQRELEDELVEELSFREQIORARQITAEQESKLENAHKSLSSTVEDLNAEI 587
      :      :      :      :      :      :      :      :      :      :
QY 366 LKTEQEKVELQHSQKQCEDDT-----VKEONFL-----YKETOFE-----KK 408
      :      :      :      :      :      :      :      :      :      :
Db 588 VSASESKELEKIH-----EAEVTWKIKLEMLEKKNNAVLDRAESQAELERLTQ 640
      :      :      :      :      :      :      :      :      :      :
QY 409 LLIISF-----PIPHPSN-----ELRGLNEMKSNKCSMLSTAEDDI 444
      :      :      :      :      :      :      :      :      :      :
Db 641 LIFSHEBELSKLKEDLEIHRINIEKLKDNLGIHYKQOIDLQNMESQKIFETMQPEKDNL 700
      :      :      :      :      :      :      :      :      :      :
QY 445 RQNTQQLPH---KNQOECILD--ISEHTISENDLE-ELRV---DHKCNIOASVHVS 493
      :      :      :      :      :      :      :      :      :      :
Db 701 ITWQOQILFISKLKDQOQSLVNSKSEEMTLQINELQKEIILRQEEKKQTLRQEOVEL 760
      :      :      :      :      :      :      :      :      :      :
QY 494 DFTDNGSQPKQKSDVYLPAPAKDKKEDLHSTFTHDSGLTTINS--SQEHLTVQAKAPF 551
      :      :      :      :      :      :      :      :      :      :
Db 761 QLKTELEKQKKEKEN-----DLQEK-----FRLQEAESILKDEKKTLEDMLKI 805
      :      :      :      :      :      :      :      :      :      :
QY 552 HTPPEEPECDKFMKMSLPS---GKIHRYKVIILGRN--RKENLEPNAEFDK-RTEFI 603
      :      :      :      :      :      :      :      :      :      :
Db 806 HTPVSGEERLIF--LDSIKSKSDSVMEKEIIELEIENEDLKQOCIOINIEIEKQRMFS 863
      :      :      :      :      :      :      :      :      :      :
QY 604 TOEEN 608
      :      :      :      :      :      :      :      :      :      :
Db 864 PAEXN 868

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RESULT 4
T30822
Impl1 protein - Mycoplasma hominis
C/Species: Mycoplasma hominis
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 07-Dec-1999
C/Accession: T30822
R/Jensen, L.T.; Ladefoged, S.; Birke Lund, S.; Christiansen, G.
Infected Immun. 63, 3336-3347, 1995
A:Title: Selection of Mycoplasma hominis pg21 deletion mutants by cultivation in the pre
A:Reference number: Z18884; MUID:95369882
A:Accession: T30822
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1365 <JEN>
A:Cross-references: EMBL:U21962; NID:g790243; PID:g790244; PIDN:AAA81013.1
C/Genetics:
A:Gene: Impl1
A:Genetic code: SGC3

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Query Match 4.9%; Score 173; DB 2; Length 1365;
Best Local Similarity 19.1%; Pred. No. 0.066;
Matches 132; Conservative 131; Mismatches 257; Indels 170; Gaps 30;

QY 19 QVKN-----EKNRPSLSKLTQDNRPKSKCKPLMGKVFYLDLPSVTISELQ----- 65
Db 231 EIKNANOAVASNNNTASMOASKS-----IDAKVAETTKRLETFNKKDKE 273
QY 66 ---KDIDLGGVVEEFLSKDISYLSNKKKEAFQOTLGRISPVPSPEASVYAEETSPHPS 122
Db 274 AKFELKQTRNQIOEFIN-----TKNNPNYSELISQLSKRDSKNSYV-----DS 319
QY 123 HDGSGFSKSPDT---VCLSRGKL-----LVEKAIKHDHDFIPNSILSNALSWGKVIILHID 173
Db 320 SNKSDIESANTKQALAKANADRVQADNLAKSIKEQ---LNNSSVSNANLISKLITDKD 375
QY 174 DIRYIIBQKKKLELV-LKSSSTSVRDSGKRVGSAQKTRIGRLLKPPKPVYEDMSQLYRPP 232

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      :      :      :      :      :      :      :      :      :      :
Db 376 NT---IQQAKTELEKEVKAQQAQATKSNNNTASMOAKSSSLAKVAE----- 417
      :      :      :      :      :      :      :      :      :      :
QY 233 YLQLTNMPFINYSIQKPCSPEDVDKPSMQKOTQYKLRQ-----TDGKGYGTSIQLO 286
      :      :      :      :      :      :      :      :      :      :
Db 418 -----ITKKLETFNKKKEAKFNLKQTRNQIOEFINTNNKPNPYSSELISQLT 464
      :      :      :      :      :      :      :      :      :      :
QY 287 LKEKKKKCYCECCLOKYEDELTHLSEOHNRNPAOSNOYQVVDIVSKIVDPPEVEKDT 346
      :      :      :      :      :      :      :      :      :      :
Db 465 SKRDSKNSVTS--SNKSDIES-ANTELKQALAKANADRVQADNLAKSI----- 510
      :      :      :      :      :      :      :      :      :      :
QY 347 KKKRKYSVGSLSVPYSAVLKK--TEQKEVELQHSQKQCEDDTQVKEQNFYKETQE 404
      :      :      :      :      :      :      :      :      :      :
Db 511 -KEQNNNSVANNTLSAKLTQDKNTIQQAKTEL-----EKEVQKQAQAIKSN-----TAS 560
      :      :      :      :      :      :      :      :      :      :
QY 405 TEKLLIFSEPIPHPSNLRGLNEMKSNKCSMLSTAEDDIRQNTQPLHKNQECILDI 464
      :      :      :      :      :      :      :      :      :      :
Db 561 MQSAKSSIDAKVAETTKLETFNKKKEAKFNLKQTRNQIOEFINTNNKPNPYSSELISQL 620
      :      :      :      :      :      :      :      :      :      :
QY 465 SEHTISENDLEELKYDHYKCNIOASVHVSDFSTDNS-----GSQPKQKSDVYLPAPAK 516
      :      :      :      :      :      :      :      :      :      :
Db 621 TSKRDSKNSVTD-----SSNKSDIESANTELKQALAKANADRVQADNL--AK 665
      :      :      :      :      :      :      :      :      :      :
QY 517 DLKREKDHISFTHDSGLTTINSQEHLLTVQAKAPRHPTPEEPECDK-FKNNDSLPSCG-- 573
      :      :      :      :      :      :      :      :      :      :
Db 666 SIKEQ-LNNSVSNANTLSAKLTQDKNTIQQAKTELEKIQKANOQATKSNNNTASMOASKS 724
      :      :      :      :      :      :      :      :      :      :
QY 574 IHRRYKVIILGRNKENLEPNAEFD--KRT-----EFTQENRIGCSSPVSILDLFQTS 626
      :      :      :      :      :      :      :      :      :      :
Db 725 LDVAVAETTKLETFNKKKEAKFNLKQTRNQIOEFINTNNK--NNYSELISQLLSK 780
      :      :      :      :      :      :      :      :      :      :
QY 627 EKSEFLGFTSTYTEKSGICNVLDIWEENSND 656
      :      :      :      :      :      :      :      :      :      :
Db 781 RDSK---NSVTDS--NKSIDI-ESANTE 802

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RESULT 5
S51441
hypothetical protein YLR309c - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein L2142.5
C/Species: Saccharomyces cerevisiae
C/Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
R/Pauley, A.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid L2142.
A:Reference number: S514437
A:Accession: S51441
A:Molecule type: DNA
A:Residues: 1-911 <PAU>
A:Cross-references: EMBL:U17247; NID:g577216; PIDN:AA867359.1; PID:g577221; MIPS:YLR3
C/Genetics:
A:Gene: SGD:IMH1
A:Cross-references: SGD:S0004300; MIPS:YLR309C
A:Map position: 12R

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Query Match 4.9%; Score 170.5; DB 2; Length 911;
Best Local Similarity 19.3%; Pred. No. 0.053;
Matches 137; Conservative 125; Mismatches 227; Indels 221; Gaps 33;

QY 54 DLPSTYISEKLQKIDKIDGVEEFLSKDISYL-----ISNKKEA-----KFAQ 97
Db 125 EIPESASSETL---KD---KEEFLKREQVYKNDIDILKMKMEALNLTPTVQKENDT 177
QY 98 TIGRISPVPSPEASVATATTSPPHSDGSSFSKSPVCLSGKLLVEKAIKHDHPIPS-- 155
Db 178 VSGLEKIVALENIILKEERAK-----KQKEVVIS--ELKEELAIKNHSGLEDSRM 226
QY 156 -----NSILSNALSWGKVIILHIDIRYIEQKKKLELYLAK-----SSTSVPDGG 200
Db 227 KITTEQLNLSKSKSTIMEKSSSELAELNLTITLKEERKLSLEKKMKLEKKAISHQVAGNN 286

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QY 201 KRVGSACKPTT--GALKPRVAVEDMSOLYRPLJOLJLNNPPLFNYSIOKPCSPDVPKPS 259
Db 287 RR-----KKNKKKKKKKKGGITTGDISE-----ELVYDNSI 317
QY 260 SMOQTOYKLAJQDGDGKYGCTSIOLOLKEKKKKGCCECLOKEDLETHU----- 310
Db 318 NNEEDKAKENIQ-----ELQEKTKD--CEDBKQKYEDEIEALDKAKLELNS 362
QY 311-----LSEOHNRPAQSN-QYQVNDYTSKLVPRPYE-----KDT 346
Db 363 QLEKSAKELETLNTELIDTKSKLKENSELEVRMDKRYQVGNELVAKKEIKESSKONE 422
QY 347 KKKRIKYSVGLSPVSAVU-----KTKQKQKVEL-----QHSQDCQEDDITYKPN 396
Db 423 EKVATYLELDRKNNKMTMEAVEANKELSKTELLSKVEYHKKUL--CTE----- 472
QY 397 FLYKETQETKEKLLIETSEPIRHPNSNELQJLNKSKNSCMSLSTAEEDIDQANTOL-PLHK 455
Db 473-----KEKEEDTQO-----NKVAKLNEI-----SOLTEKNTIKELTSLKTSYK 513
QY 456 NKQECILDISHT-----LSENDLEBLRVHYKONIQ-----ASHVSDFTDN 499
Db 514 QKEKTVSYLEQVAKQFSEQKQDAVEKSTEDQKRDIAKJSNRDLDKKENETLINDIAKNSN 573
QY 500 SCSOPKQSDTVLEPANDLKEK--DLHSITFHDSGL--TJNSQEHUJYQAKAPRHPPE 556
Db 574 SYEEELKNGKLSERLNIQEKYNTLQNVKSSNBEHDSIKROCEELANVLE----- 626
QY 557 EPNEDECFNMDSLPFGKIHKKVJILGNRRKENL-----EPNAEDKRTETI 603
Db 627-----STKKILST--EDLLENYANIVODKTRCNTLRRLRVSDQSDSSQKOLEKKAIVL 680
QY 604 TOENRICKSPVQSLDLFQTSSEKSEFLGPT--SYTEKSGICVNDIMEE 652
Db 681 TEKKNKU-----EAEIDL--QTSKRATELOEKMHVTVTELKSEIHALKLEEE 724

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QY 200 GRVVGAGKRTGTGLKRPVKVEJMSOLRPFLOJOTNPFINTYISQKPCSPFDVKPS 259
Db 790 -----KKNYKNNNDSN--KTFELKIEN-----810
QY 260 SMOKQOVKLRJOTQGDYRGSTJOLQJLKEKKKGYCEQJCK-----YEDLPTHLS 312
Db 811 -----EFKDILLDSQJFGDSJLADIKE--YNTADMLDNNNENKSLYEDGENFIT- 860
QY 313 EOHNRNAGSNQOVWDIVYSKLYPDEVYE-----KDPKRRIRYSGSISPVASAYL 366
Db 861 ---RNEPITNEBERNNIT--YISDEQYNEEDLIFMDKIKERKKNNDPSSDPFENGQVQ 915
QY 367 KTEQKEKVELQIHISQKQCOEDDTTVKQONLKYETQET--KLLFISEPIHPSNEL 423
Db 916 EKIYVNEKILBEYNKNDKSSSSSSIIIEETIKYKKNEDLVPALCYLIDEPH-SNDL 974
QY 424 RGINEKMSKCSMLSTAEDDIRONFTQLPLHKNKQECILDISHTLS---ENDLEELVD 480
Db 975 EN-----NTISVSSDDMKTN-----VSKNNITGYKKNKVDITANE 1009
QY 481 HYKCNIOASHVSDSTDNSSQPKQKSDTVLPAKDLKEDLHSTFTDGLGILTNS-- 538
Db 1010 YDKKGDGVLEIS-FEDSKRLEESKFPDDNNNIYDNDELKRLSKOTISDVDRKNHNNIY 1068
QY 539 -----SOEHITVQAKAFHTPREPNE--C-----DFKNMDSLPSGKIH 575
Db 1069 NIERGEDERENENVEKNKIO-STESHKRSNEFITCENKSLRKQYMSKEDISNVRKLSSDIN 1127
QY 576 RKVK-----ITLGR-----NRKENLEPNAE-----FDKRTFTTQENBRICSSPVQSTL 619
Db 1128 NLSQNYFELLDRKQVMDNFQMNIEQNNNDKLKEDKLDECAVEYLEDNKKITIDSYIK--- 1184
QY 620 DLFQTSBEKSEEPJGFTSYTEKSGICQNVLDIWEENSD-NLLTAFESP 666
Db 1185 ---ETKNENDELLIKRYKRLK---NNTIENDENNDKIKLLNFFGIP 1225

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RESULT      6
E71619
RAD2 endonuclease PFB0265c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #ext_change 21-Jul-2000
C:Accession: E71619
R:Gardner, M.J.; Tetteh, H.; Carnucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
R.: Pereira, M.; Salzberg, S.; Zhou, L.; Dutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: E71619
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1516 <GAR>
A:Cross-references: GB:AE001363; GB:AE001362; NID:93845335; PIDN:ACG71842.1; PID:9384511
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0265c

Query Match      4.8%; Score 170; DB 2; Length 1516;
Best Local Similarity 19.5%; Pred. No. 0.11;
Matches 138; Conservative 115; Mismatches 257; Indels 198; Gaps 31;

29 LKSLKTDNPEKSKCKPLMCKVFFYLDLPSTVITSEKLR-----DIKLDGGRVFEFLSKD 82

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RESULT 7
 D96796
 probable heat shock protein, 53413-59028 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: D96796
 R:Thellogiannis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408: 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luero, J.S.; Maltl, R.; Marzita
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, S.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID: 21016719
 A:Accession: D96796
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 11871 <STO>
 A:Cross-references: GB:AE005173; NID:96143906; PIDN:AAF04452.1; GSPDB:GM00141
 C:Genetics:
 A:Gene: F28016.15
 A:Map position: 1

```

Query Match 4.8%; Score 170; Db 2; Length 1516;
Best Local Similarity 19.5%; Pred. No. 0.11;
Matches 138; Conservative 115; Mismatches 27; Indels 198; Gaps 31;

QY 29 LKSLKTDNRPEKSKCKPLMGKVFYLDLPSTVTSLEKQ-----DKIDAGKVEEELSKD 82
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 646 VRIKTDPEIKELKLIK-----MAENIQSVBEELLINKDLSKNTMDINIKD 690

QY 83 ISYL--ISNKKKAKFQOTLCRIISPVPSPESAYTAEITSPHPSIDSSKRSPTYCLSRG 139
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 691 YNLOKKRSKKKKKKFLNDI-----LNTYNTTSSKTKODLYAKGEESKDI-KNQT 740

QY 140 KLIVKKAIKDHQFIPSPNISLNAISMGVKILHIDIRYIEOKKRELYLILKRSSTSVRGD 199
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 741 DFTYQCCYNNNDIIRDTHDKSDF--KNIKD-----NKKRYEYLYNLEQEEIN- 789

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```
Query Match      4.7%   Score 166.5; Db 2; length 187;  
Best Local Similarity    20.2%; Pred.No. 0.23;  
Matches 148; Conservative 109; Mismatches 267; Indels 207; Gaps 33;
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Oy 17 GIOVKNENRPSLSKSTIDNRREKRCKPLW---GRVFYLDLSPVTISEK-----IQDKI 68
|| : :::: | : : : : || : : : :
Db 907 GIF-EHMLHPRIKHEDRRNNRVYGAK-EPISOEGKEERKELVESMTITENDNSIDVOETRK 964

QY 591 --EPNAEDKRTTEPT--QENNRICSSPVOSLIDLFQTSSEK-----SEFLGFTSYTEKS 641
Db 533 CNKMKDEEDKKNNSNNEEENIILDSKEQNI--ILDINKELKLSKEKKKKIKSIKIKKT 590
QY 642 GICNVLDIWEENSNDL 658
Db 591 KIEDNKDIKENENFNEI 607
RESULT 11
T28677
Rhoptry protein - Plasmodium yoelii
C:Species: Plasmodium yoelii
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T28677; C45521
R:Keen, J.; Slaha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A:Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii.
A:Reference number: 220508; MUID:95021522
A:Accession: T28677
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2269 <KEE>
A:Cross-references: EMBL:L27838; NID:9457145; PID:9457146; PIDN:AAA21304.1
R:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A:Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple cc
A:Reference number: A45521; MUID:91101660
A:Accession: C45521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 2131-2269 <KE2>
A:Cross-references: GB:M34283

Query Match 4.6%; Score 162; DB 2; Length 2269;
Best Local Similarity 17.4%; Pred. No. 0.53; Mismatches 289; Indels 266; Gaps 34;
Matches 149; Conservative 152;
QY 9 HSKGHFQGIQVKNKNSPSKSLKTDNRPEKSK-----CKPLMGKVF 51
Db 1085 NEKIHEDV--ANNDSKNAKITSIVSEPFKTLIKINEIRKSDDCIKETNDLEKQIS 1143
QY 52 YLDLPS-----VTISF-----KLQKIDKJAGRYEELLS--KDISYIISNKK 91
Db 1144 NLSIDTQETKLTENGKQKLTLEELLESKKOKKNEDOKKLEDEVNSIKNIENVTNQHKK 1203
QY 92 ---EAKFNQITGRISPVSPESAVTAETTSPPHSDGSSFPDVTCL---SRGKLIVE 144
Db 1204 KNYEIGYKEKINEIAKTKNNOESTKELKPTIQHITSSFNANDLEGIDSDENLGRKVTTE 1263
QY 145 KAIKDHPFIPNSILSNALSMGVK-----IIHIDDIRY-----YI 179
Db 1264 MGNIEEFIKSVNLNTNLEFYSKESITYNOTQNKRIDTQKELKNIENVNAKSYLDYI 1323
QY 180 EOK-----KKELLYL-----KKSSTSVRDGKRVGSGAOKTYTGRLKPFVVEDMS 226
Db 1324 KENEDRIVTTHFKKLTNVNDFKNKNEYSKVNKGFDNISITFVNSTDENSILNINOT 1383
QY 227 QLYRPFYQLTNMPFINSIO-----KPCSPFDVDP----- 258
Db 1384 ---KEMVANIYNNNTYISKYELENIFRNIPKLANTLNLIKIKSSGIDLSKDIKIAILSYL 1440
QY 259 ---SSMOKOTQVKLRIQTDGKYGTSIOQLKKEKKKGYCECCLQKYEDEL 307
Db 1441 DSKETEDLFIIPSPQKKTETETKI---SDSY---SILDLILKSGE-----LQKKEQGT 1488
QY 308 THLSQHRNNA-----OSNO-----YQVVD 329
Db 1489 LKLIFENRRLYEKVQATNELRGTLSDLYKKKKILSEYKLLLHKKSNEILKLSNCFQNYDT 1548
QY 330 IYSKLVFDPVEVEKKTTPKKR---IKYSVGSLSPVASVYLKKTQKKE----- 373

Db 1549 ILESKDYQVKEKSNNYKOEKELGIDFNVTDMEEKFNNDIKVIELEENNNYSEENNMI 1608
QY 374 ---KYELOHISK---DQEDDTYKQNFYKQEPTEKILLFSEPIPHSPNLRGIN 427
Db 1609 LOSKOKLEKLTNKNFAETKIDDKITTEKNDLIDKLIETFRKNOMLTH-----TTLAETIK 1663
QY 428 EKMSNKGSMLSAEDDIDNQTPLPHKKNKOCILDISHTLSEND---LEELRYDHYKC 484
Db 1664 IKITDYSKFIESAT-----KFSKEFLYITGDTSLNDDIATLOLKTIDHDI 1710
QY 485 NIQASVHVSDFSTNDSGSPKQKSDTVLEPAKOLKEKDLHSITFDHSGLLITNS--SQEH 542
Db 1711 NKYVTSKLSDATNDNNNLIKEKEKATQAI-----KNLTFTLIDSNIDANALHNKI 1763
QY 543 LTVQAKAPEHTTPPEPNECDFFKNMDSLPSGKTHKVKII---LGRNKENLEPNAEPK 598
Db 1764 QMVYVNSLH-----KSIESIK--QLYKKMHVFKLLNIQINQKYPDISKQFDN 1810
QY 599 PTEFTQEFNRICSSPVOSLIDLFQ-TSREKSEFL-----GFTSYTE-----K 640
Db 1811 ---ILQLOESELTNLNDLKEIGOKISDKNNKFLHALNETPIPNFTYKLEYHDIYK 1866
QY 641 SGICNVLDIWEENSND 656
Db 1867 RQIDELIENTSEENEN 1882

RESULT 12
153799
CGI protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: 153799
R:Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.
Gene 144, 221-228, 1994
A:Title: Cloning of a gene encoding a human leukocyte protein characterised by extens
A:Reference number: 153799; MUID:94314220
A:Accession: 153799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1300 <RES>
A:Cross-references: GB:L25616; NID:9409465; PIDN:AB65853.1; PID:9409466
C:Genetics:
A:Gene: GDB:CG1
A:Cross-references: GDB:450341
Query Match 4.6%; Score 161; DB 2; Length 1300;
Best Local Similarity 20.2%; Pred. No. 0.29; Mismatches 279; Indels 172; Gaps 34;
Matches 147; Conservative 130;
QY 17 GIOVNEKNRPSLKLKTDNRPEKSKCPPLMGKVFYLDLPSYISEKLOKDKIDL---G 72
Db 262 GIO-----KSGTKKLTKTETDKENAEVK---FKDFLISLKTMMFSDALCVVDLKEKS 312
QY 73 GRVEEFLSK---DISYLSNKKKAFAOTLCRISPVSPESAVTAETTSPPHSDGSSF 128
Db 313 GVIODALKSKSGEFTTLHLOLEKD--KLAAVK-----EDAAATKDRCKOLOTEMKTE 365
QY 129 KSPDNYCISRGKLVLEKAKHDHFIPIINSILSNALSMGVKIIHIDIRYIIOKKKLEL 188
Db 366 KERSNVITTRMDRIGTLKEKHNVPONKTHVSYQETQOQK--MKFOOVR---BQMELEIHA 421
QY 189 LKKSSTSVBDGKRVGSGAOKRTGRKLPKPFVVEDMSQLYRPFYQLTNMPFINSIOK 248
Db 422 LKQENGILBDVANSNTNNGESQSAELNK-----LRQDVARIYNELTEK---TGKIQ 471
QY 249 PCSPPDYDKPSSMOKOTQVKLRIQTDGKYGTSIOQLKKEKKKGYCECCLQKYEDEL 308
Db 472 E---EVOCKKNAEOAATOLKVOLOEAERWE---EVOQYIRKRAEHBAQO---DIQS 520
QY 309 HLTSQHRNFAQSNQYQVVDIVSK---LVEDFVEYE--KDTPPKKRRIKYSVGSLSL--- 358

Db 521 KEVAK--NEVOSLSKLTDTLVSKOOLEORLMQIMSEBOKRVNKEESLOMOVODILEON 578
 QY 359 -----SPVSASVY-----KTEOKEREVLQHSQDCQED 388
 Db 579 EALKAQIOFHQAOTASVLAELHVKYIAEKDKQIKQETEDSLASERDLTSK--EE 636
 QY 389 DTTVEQOFLTK-ETQTEKKLFTSEPIPHPSNELRGLENKSNKCSMLSTAEDDIRON 447
 Db 637 LKDIQNNFLAKAEVQ-----KLQALANEOAAAHEL-----EKMOOS---VYVADDKIRLL 685
 QY 448 FTQPLHKNKQECCLIDISEHTLSENDLEELRV--DHYKCNIOASVH-----VSDFTDMS 500
 Db 686 EEOU-----QHEIS-NKMEEFKILNDONKA-LKSEVQKLOTLVSEOPKNDV 729
 QY 501 GSOPK---QKSDTVLFPAKDKLEKDLHSIFTHDSGLITINSQOEH/VQAKAPHTPPEE 557
 Db 730 VEOMKCTIOEKDEKLTVELELTGLIOVATKEBELNAIRTESSLT-----KE 778
 QY 558 PNECDFKNMDSLPSCGIHRKVIILG-----RNKENLEPN---AEFDKRTETIOE- 606
 Db 779 VODLKAQNDQVSPASVLEELKVIHEKDKIKSVLEELAEELLVANKERTVODLKQEI 838
 QY 607 -----ENRICSPVOSLIDLFTQSEKSEFLGTSTYKSGICN---VL 647
 Db 839 KALKEIGNVQLEKAQOLITSKYOELONLKGEBOHMTKAVLEEKEDLANGTGKWLQ 898
 QY 648 DIWEFENS 655
 Db 899 DLOEENES 906

RESULT 13
 S32763
 Kineclin 1 - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S32763; 137947
 R:Kruppa, G.; Fuetterer, A.; Lemke, H.; Kromeke, M.
 submitted to the EMBL Data Library, April 1993
 A:Description: Cloning and characterization of TAF, a novel transactivating protein.
 A:Reference number: S32763
 A:Accession: S32763
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1356 <NRU>
 A:Cross-references: EMBL:222551
 R:Futterer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kromeke, M.
 Mol. Biol. Cell 6, 161-170, 1995
 A:Title: Molecular cloning and characterization of human kineclin.
 A:Reference number: 137947; MUID:95306853
 A:Accession: 137947
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1356 <RES>
 A:Cross-references: EMBL:222551; NID:9296163; PIDN:CAAB0271.1; PID:9296164
 C:Genetics:
 A:Gene: GDB:KTN1
 A:Cross-references: GDB:6165852; OMIM:600653

Query Match 4.6%; Score 161; DB 2; Length 1356;
 Best Local Similarity 20.2%; Pred. No. 0.3; 279; Indels 172; Gaps 34;
 Matches 147; Conservative 130; Mismatches 17; Indels 172; Gaps 34;
 QY 17 GIQVKNENKPSLSKLTQNRPEKSKCPPLMGKVFYLDLPSTVISEKLOKIDL----G 72
 Db 261 GIQ-----KSGTKIKTETEDKNEAEV---FKDFLLSLKTMFSEDEALCVADLTKRS 311
 QY 73 GRVSEPLSK-----DYLISNKKKAKFAOTLGRISPVSPESAVYTFETTSPPHSDGSSF 128
 Db 312 GVIDALKKSSKSELITLILHQLQKMD--KLAAVK-----EDAAATKRCRQLOLTQEMATE 364
 QY 129 KSPOTVCLSKGLLVEKAIKDHDFIPNSIISNLSMGVILHIDDIRYIIOKKKELYL 188

Db 365 KERSNVNTRMAKDRIGTLEKHNVFQNKIHVSQETQOMQ--MKFOYR---EQMEAEIAH 420
 QY 189 LKRSSTVSDGSKRVGSAQKTRTGKLRKPFYKVEDMSQLRPFYQLQTMPPINTSIOK 248
 Db 421 LKQENGLIDAVSNITTMQLESKQAEALNK-----LQDVARLVNELTEK---TGKLDQ 470
 QY 249 PCSFPVDKPSMOKQVYKLRITQDGGTSTIOLQLEKKKKGCECCLOKXYDELTE 308
 Db 471 E---EVQKRNQEAQATQKVOLOEABRWME---EVQSYIKKRAHEAQAQ---DLOS 519
 QY 309 HLSEQRHNPFAOSNOYQVVDIVSK-----LVDFVEYB-KTPPKKRIKYSVGL- 358
 Db 520 KEVAK--NEVOSLSKLTDTLVSKOOLEORLMQIMSEBOKRVNKEESLOMOVODILEON 577
 QY 359 -----SPVSASVY-----KTEOKEREVLQHSQDCQED 388
 Db 578 EALKAQIOFHQAOTASVLAELHVKYIAEKDKQIKQETEDSLASERDLTSK--EE 635
 QY 389 DTTVEQOFLTK-ETQTEKKLFTSEPIPHPSNELRGLENKSNKCSMLSTAEDDIRON 447
 Db 636 LKDIQNNFLAKAEVQ-----KLQALANEOAAAHEL-----EKMOOS---VYVADDKIRLL 684
 QY 448 FTQPLHKNKQECCLIDISEHTLSENDLEELRV--DHYKCNIOASVH-----VSDFTDMS 500
 Db 685 EEOU-----QHEIS-NKMEEFKILNDONKA-LKSEVQKLOTLVSEOPKNDV 728
 QY 501 GSOPK---QKSDTVLFPAKDKLEKDLHSIFTHDSGLITINSQOEH/VQAKAPHTPPEE 557
 Db 729 VEOMKCTIOEKDEKLTVELELTGLIOVATKEBELNAIRTESSLT-----KE 777
 QY 558 PNECDFKNMDSLPSCGIHRKVIILG-----RNKENLEPN---AEFDKRTETIOE- 606
 Db 778 VODLKAQNDQVSPASVLEELKVIHEKDKIKSVLEELAEELLVANKERTVODLKQEI 837
 QY 607 -----ENRICSPVOSLIDLFTQSEKSEFLGTSTYKSGICN---VL 647
 Db 838 KALKEIGNVQLEKAQOLITSKYOELONLKGEBOHMTKAVLEEKEDLANGTGKWLQ 897
 QY 648 DIWEFENS 655
 Db 898 DLOEENES 905

RESULT 14
 A43336
 microtubule-vesicle linker CLIP-170 - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: A43336
 R:Pierre, B.; Scheel, J.; Richard, J.E.; Kreis, T.E.
 Cell 70, 887-900, 1992
 A:Title: CLIP-170 links endocytic vesicles to microtubules.
 A:Reference number: A43336; MUID:92405160
 A:Accession: A43336
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1392 <PIE>
 A:Cross-references: GB:M97501; NID:9180621; PIDN:AAA35693.1; PID:9180622

Query Match 4.5%; Score 159.5; DB 2; Length 1392;
 Best Local Similarity 17.3%; Pred. No. 0.38;
 Matches 127; Conservative 137; Mismatches 295; Indels 175; Gaps 28;
 QY 11 KGHFGGQGVN-----EKNRPSLSKLTQNRPEKSKCPPLMGKVFYLDLPSTVISEKLO 65
 Db 735 KASSEKSEBKKLQOUELAERKQIKHLERKNAESSKASTRELQGRLEKLTNLQENIS 794
 QY 66 KDIDKIDGRVDEFTLSKIDSYLISNKKKAKFAOTLGRISPVSPESAVYTA-----ETTSP- 119
 Db 795 E-----VSQVKELEKELQITL-----KEKFAE-----ASEEAVSVQSRMDETIVNKL 835

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